Please amend the application as follows:

In the claims:

Please cancel claims 1-11 without prejudice or disclaimer as drawn to non-elected inventions.

Please add the following new claims:

12. A method for generating a secondary library of scaffold protein variants comprising:

a) generating a probability distribution table of amino acid residues in a plurality of variant positions utilizing a force field calculation; and

b) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences;

wherein at least one of said secondary variants is different from said primary variants.

13. A method according to claim 12, wherein said force field calculation is SCMF.

14. A method according to claim 12, further comprising computationally recombining said secondary library to generate a tertiary library.

15. A method according to claim 14, wherein Protein Design Automation (PDA™) is used to recombine said secondary library.

16. A method for generating a secondary library of scaffold protein variants comprising:

a) generating a probability distribution table of amino acid residues in a plurality of variant positions utilizing an alignment program;

b) combining a plurality of said amino acid residues to g nerate a secondary library of secondary sequences, wherein at least one of said secondary variants is different from

said primary variants; and

c) computational ranking said secondary library.

17. A method according to claim 16, further comprising computationally recombining said secondary library to generate a tertiary library.

18. A method according to claim 17, wherein PDA™ is used to recombine said secondary library.

19. A method according to claim 16, wherein said alignment program is a sequence alignment program.

20. A method according to claim 16, wherein said alignment program is a structural alignment program.

21. A method according to claims 12 or 16 further comprising synthesizing a plurality of said secondary sequences.

22. A method according to claim 21 wherein said synthesizing is done by multiple PCR with pooled oligonucleotides.

23. A method according to 22 wherein said pooled oligonucleotides are added in equimolar amounts.